

SEARCH REQUEST FORM

4-777

Examiner # (Mandatory): _____ Requester's Full Name: _____

Art Unit _____ Location (Bldg/Room#): 10E03 Phone (circle 305 306 308) _____

Serial Number: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

Title of Invention _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Keywords (include any known synonyms registry numbers, explanation of initialisms): _____

Search Topic:

Please write detailed statement of the search topic, and the concept of the invention. Describe as specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc., if known. You may include a copy of the abstract and the broadcast or most relevant claim(s).

STAFF USE ONLY

Searcher: PROB

Searcher Phone #: _____

Searcher Location: _____

Date Picked Up: _____

Date Completed: 5-6-99Clerical Prep Time: 25Terminal Time: 50Number of Databases: 11

Type of Search

3 N.A. Sequence5 A.A. Sequence

____ Structure (#)

____ Bibliographic

____ Litigation MP, Confusion

____ Fulltext

____ Procurement

____ Other

Vendors (include cost where applicable)

____ STN

____ Questel/Orbit

____ Lexis/Nexis

____ WWW/Internet

____ In-house sequence systems (list)

____ Dialog

____ Dr. Link

____ Westlaw

____ Other (specify)

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 5, 1999, 07:26:47 ; Search time 36.08 seconds
(without alignments)
281.351 Million cell updates/sec

Title: US-09-037-460-2

Perfect score: 918

Sequence: 1 MKSVLLTLLVPAHLVAAM.....EVVKNAGSPVVRKWLNPR 184

Scoring table: PAM150

Searched: 180763 seqs, 55169189 residues

Database :

- SPTREMBL.8:*
1: sp_fungi:*
2: sp_human:*
3: sp_invertebrate:*
4: sp_mammal:*
5: sp_mhc:*
6: sp_organelle:*
7: sp_phage:*
8: sp_plant:*
9: sp_bacteria:*
10: sp_rodent:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_unclassified:*
14: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	918	100.0	184	2	Q15330	Q15330 homo sapien
2	698	76.0	184	10	P97682	P97682 rattus norv
3	131	14.3	1574	10	O88281	O88281 rattus norv
4	123.5	13.5	480	2	Q92743	Q92743 homo sapien
5	111	12.1	220	10	Q63404	Q63404 rattus norv
6	113.5	12.4	830	2	Q14162	Q14162 homo sapien
7	113.5	12.4	830	2	O43701	O43701 homo sapien
8	110.5	12.0	381	2	O43775	O43775 homo sapien
9	109	11.9	250	2	O76076	O76076 homo sapien
10	100	10.9	343	12	O42607	O42607 xenopus lae
11	98	10.7	251	3	Q24774	Q24774 enchytraeus
12	97.5	10.6	367	10	O54775	O54775 mus musculus
13	98.5	10.7	1116	12	O73791	O73791 brachydanio
14	97	10.6	1792	12	O57484	O57484 gallus gall
15	96.5	10.5	1645	2	O15230	O15230 homo sapien
16	89.5	9.7	281	10	O88812	O88812 mus musculus
17	95	10.3	1725	10	P70570	P70570 rattus norv
18	94	10.2	1816	10	P97927	P97927 mus musculus
19	83	9.0	153	2	O75095	O75095 homo sapien
20	88	9.6	728	12	Q90656	Q90656 gallus gall
21	84.5	9.2	282	2	Q16270	Q16270 homo sapien
22	79.5	8.7	88	8	Q43666	Q43666 triticum ae
23	85	9.3	547	10	P97881	P97881 rattus norv
24	91.5	10.0	3704	3	P91904	P91904 caenorhabdi
25	81.5	8.9	277	2	Q07822	Q07822 homo sapien
26	80	8.7	190	12	O93518	O93518 gloydius ha
27	83	9.0	471	4	O19131	O19131 bos taurus
28	85	9.3	955	2	O93466	O93466 homo sapien
29	87.5	9.5	2212	2	Q93072	Q93072 homo sapien

30	82	8.9	530	3	Q24526	Q24526 drosophila
31	78	8.5	169	2	Q14564	Q14564 homo sapien
32	75.5	8.2	88	8	Q43663	Q43663 triticum ae
33	84	9.2	1106	3	Q17494	Q17494 caenorhabdi
34	82	8.9	789	10	P70505	P70505 rattus norv
35	80	8.7	452	2	O60295	O60295 homo sapien
36	85	9.3	1999	2	Q99940	Q99940 homo sapien
37	85	9.3	2003	2	O00306	O00306 homo sapien
38	76.5	8.3	176	3	Q16364	Q16364 caenorhabdi
39	75	8.2	149	3	O46176	O46176 aedes aegypt
40	80	8.7	727	3	Q94528	Q94528 drosophila
41	78.5	8.6	518	2	Q14810	Q14810 homo sapien
42	78.5	8.6	524	2	Q14808	Q14808 homo sapien
43	75	8.2	195	3	Q18805	Q18805 caenorhabdi
44	79.5	8.7	719	2	O60283	O60283 homo sapien
45	79.5	8.7	748	4	Q10741	Q10741 bos taurus

ALIGNMENTS

RESULT 1

Q15330 PRELIMINARY; PRT; 184 AA.
AC Q15330
ID Q15330
AC Q15330
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ESM-1 SECRETORY PROTEIN PRECURSOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96355375.
RA LASSALLE P.M., MOLET S., JANIN A., VANDER-HEYDEN J.E., TAVERNIER J.,
RA FIERS W., DEVOS R.E., TONNEL A.E.B.;
RT "ESM-1 is a novel human endothelial cell-specific molecule expressed
in lung and regulated by cytokines";
RL J. BIOL. CHEM. 271:20458-20464(1996).
DR EMBL; X89426; E189266; -
DR PFAM; PF00219; IGFBP; 1.
KW SIGNAL.
FT SIGNAL
FT CHAIN 1 19 POTENTIAL
SQ SEQUENCE 184 AA; 20095 MW; 08D109DF CRC32;
ESM-1 SECRETORY PROTEIN.

Query Match 100.0%; Score 918; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 4e-93; 0; Indels 0; Gaps 0;
Matches 184; Conservative 0; Mismatches 0;

QY	1	MKSVLLTLLVPAHLVAAMNNYAVDCPHQCDSSCKSPRCKRTVLDGCGCRVCAAG	60
Db	1	MKSVLLTLLVPAHLVAAMNNYAVDCPHQCDSSCKSPRCKRTVLDGCGCRVCAAG	60
QY	61	RGFTCYRTVSGMDGKCGGLRQCPNGEDPGEFGICKDCPYGTFGMDCRETNCQSG	120
Db	61	RGFTCYRTVSGMDGKCGGLRQCPNGEDPGEFGICKDCPYGTFGMDCRETNCQSG	120
QY	121	ICDRGTGKCLKPFFFOYVTKSSNREVSLETHDMSGDCGNIVREEVVKNAGSPVVRKW	180
Db	121	ICDRGTGKCLKPFFFOYVTKSSNREVSLETHDMSGDCGNIVREEVVKNAGSPVVRKW	180
QY	181	LNPR 184	
Db	181	LNPR 184	

RESULT 2

P97682 PRELIMINARY; PRT; 184 AA.
ID P97682
AC P97682

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DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE PG25.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY; TISSUE-PINEAL GLAND;
RA WANG X., BROWNSTEIN M.J., YOUNG W.S.;
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U08018; G1750198;
SQ SEQUENCE 184 AA; 20075 MW; 3457564C CRC32;

Query Match 76.08; Score 698; DB 10; Length 184;
Best Local Similarity 74.18; Pred. No. 4.4e-69;
Matches 137; Conservative 24; Mismatches 22; Indels 2; Gaps 2;

QY 1 MKSVLLTLLVPAHLVAWSNNYAVDCPOHCDSECKSSPRCKRTVLDGCGCRVCAAG 60
Db 1 MKSVLLTLLVPAHLVAWSNNYAVDCPOHCDSECKSSPRCKRTVLDGCGCRVCAAG 60
QY 61 RGCTCYRTVSGMDGKCGPLRGKCPNGEDPFGBEFGICKDCPYGTGMDCRETNCQSG 120
Db 61 PGCTCYRTVSGMDGKCGPLRGKCHFYSEDDFGDFGVCKDCPYGTGMDCRETNCQSG 120
QY 121 ICDRGTKCLFPFFQSVTKSNR-FVSLFHDHMASGDGNVREVVYKNAAGSPVNRK 179
Db 121 ICDRVTCGLDFPFQYAAKSPSRTSASQTERDAASGDGNVREIEIGDRNAARPSVM-K 179
QY 180 WLNPR 184
Db 180 WLNPR 184

RESULT 3
QY 088281 PRELIMINARY; PRT; 1574 AA.
AC 088281;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MEGF6.
GN MEGF6.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RA NAKAYAMA M., NAKAJIMA D., NAGASE T., NOMURA N., SEKI N., OHARA O.;
RT "Identification of high-molecular-weight proteins with multiple
EGF-like motifs by motif-trap screening.";
RL GENOMICS 51:27-34(1998)
DR EMBL; AB011532; D1033425;
DR PROSITE; PS00010; ASX-HYDROXYL; 5.
DR PROSITE; PS01186; EGF-2; 23.
DR PROSITE; PS01187; EGF-CA; 5.
KW GLYCOPROTEIN; EGF-LIKE DOMAIN.
SQ SEQUENCE 1574 AA; 165445 MW; C49E6EA6 CRC32;

Query Match 14.38; Score 131; DB 10; Length 1574;
Best Local Similarity 23.98; Pred. No. 2.5e-06;
Matches 37; Conservative 23; Mismatches 23; Indels 72; Gaps 9;

QY 15 HLVAWSNNYAVDCPOHC-----DSSSECKS---SPRCKRVLDGCGCRVCAAG 52
Db 642 HLACPPWA--FGPGCSDELCLCEOSHTRSCNPKDGSCSKAGFQGCQ-----AECESGFF 695
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QY 52 --GCRVCAAGRGETCYRTVSGMDGKCGPLRCQPSNGEDPFGEEFGICK-----101
Db 696 GPGCRHCT-----CQFGVACDPVSGE-----CRTQCPPGYQG 728
QY 101 -----DCPYGTGMDCRETNCQSGICDRGTGKCL 130
Db 729 EDCQCECPVGTGFGVNCSCGSCVCGAPCHRVGTGCL 763

RESULT 4
QY 092743 PRELIMINARY; PRT; 480 AA.
AC 092743;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE NOVEL SERINE PROTEASE.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 97131593.
RA ZUMBRUNN J., TRUEB B.;
RT "Primary structure of a putative serine protease specific for
IGF-binding proteins.";
RL FEBS LETT. 398:187-192(1996).
DR EMBL; Y07921; E275186;
DR PFAM; PF00050; kazal; 1.
DR PFAM; PF00089; trypsin; 1.
DR PFAM; PF00219; IGFEP; 1.
DR PFAM; PF00595; PD2; 1.
KW PROTEASE; SERINE PROTEASE.
SQ SEQUENCE 480 AA; 51286 MW; 175BB6D9 CRC32;

Query Match 13.58; Score 123.5; DB 2; Length 480;
Best Local Similarity 34.08; Pred. No. 5.8e-06;
Matches 33; Conservative 18; Mismatches 25; Indels 21; Gaps 5;

QY 4 VLLITLLVPAHLV-AAWSNNYAVDCPQHCDSECKSSP-----RCKRTVLDGCGCRV 56
Db 12 LLLLLAAPASAOQLSRAGRSAPLAAGCPDRCEPARCPQPEHCEGGRAR-----DACGCEV 67
QY 57 CAAGRETCTYRTVSGMDGKCGPLRCQPSNGEDPFG 93
Db 68 CGAPEGAAAC-----GLOEGPGEGLOCVV-----PFG 94

RESULT 5
QY 063404 PRELIMINARY; PRT; 220 AA.
AC 063404;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE (CLONE REM4) ORF (FRAGMENT).
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HOLZMAN; TISSUE-BRAIN;
RX MEDLINE; 96235155.
RA ASAKURA K., POGULIS R.J., PEASE L.R., RODRIGUEZ M.;
RT "A monoclonal autoantibody which promotes central nervous system
remyelination is highly polyreactive to multiple known and novel
antigens.";
RL J. NEUROIMMUNOL. 65:11-19(1996).
DR EMBL; L41686; G780367;
DR PROSITE; PS01186; EGF-2; 5.
DR PFAM; PF00008; EGF; 3.
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us-09-037-460-2.ispt

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; CARNIVORA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RE [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HEN;
RK MEDLINE: 98119879.
RA HASHIMOTO Y., TOMA H., YOKOTA J.;
RA SHIROISHI T., TOMA H., YOKOTA J.;
RT "Expression of the Elm1 gene, a novel gene of the CCN (connective
RT tissue growth factor, Cyr61/Cef10, and neuroblastoma overexpressed
RT gene) family, suppresses in vivo tumor growth and metastasis of K-1735
RT murine melanoma cells.";
RL J. EXP. MED. 187:289-296(1998).
DR EMBL: AB004873; D1025874;
DR PROSITE; PS01185; CTCK.1; 1.
SQ SEQUENCE 367 AA; 40702 MW; 1AB35AB9 CRC32;

Query Match 10.6%; Score 97.5; DB 10; Length 367;
Best Local Similarity 28.2%; Pred. No. 0.0032;
Matches 35; Conservative 15; Mismatches 35; Indels 39; Gaps 10;
QY 27 DCPQHCDSECKSSPRCK---RVVLDDCGCCVCAAGRGTCYRTVSGMDGKCGP--GL 81
DB 54 ECPQ-----SPPCPLGVSILITDCCECKICAQQLGDC-----TEAICDPHRL 99
QY 82 RQPSNGEDPFGEEFGICKD-----C-----PY-----GTFGMDCRETCNCSGI--CDRGT 126
DB 100 YDYSDDPRYA--IGVCAOVGVGVLDGVRYTNGESFPNCRYNCTIDGTVC---T 154
QY 127 GKCL 130
DB 155 PLCL 158

RESULT 13
O73791
ID O73791 PRELIMINARY; PRT; 1116 AA.
AC O73791;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE ENDOTHELIUM-SPECIFIC RECEPTOR TYROSINE KINASE TIE-2.
GN TIE-2.
OS BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
RN [1]
RP SEQUENCE FROM N.A.
RA LYONS M.S., BELL B., STAINIER D., PETERS K.G.;
RL DEV. DYN. 0:0-0(1998).
DR EMBL: AF053632; G3005607;
SQ SEQUENCE 1116 AA; 122361 MW; 7E60F6C5 CRC32;

Query Match 10.7%; Score 98.5; DB 12; Length 1116;
Best Local Similarity 23.7%; Pred. No. 0.0066;
Matches 36; Conservative 18; Mismatches 33; Indels 65; Gaps 8;
QY 7 LTTLLVPAHLVAANNVAVDCPQCHDSSECKSSPRCKRTVLDGCGCRVCAAG--RGETC 65
DB 207 ITRLIVSRAGFWGPNCTSCPCANGGVCDT-----GEC-----VCPGFRGHTC 255
QY 66 YRTVSGMDGKCGP-----LRCQPSNGEDPFGEEFGIC----- 100
DB 256 -----DIVCGEGRGAGKERCVDGVCAALVFLR-----DPYG-----CSCASG 295
QY 100 -----KDCPYCTFGMDCRETCNCSGICDR 124
DB 296 WRGLSCNDACPDGYYGAGCTQKCVCAKGRCDR 327

Query Match 10.6%; Score 97; DB 12; Length 1792;
Best Local Similarity 23.0%; Pred. No. 0.015;
Matches 43; Conservative 22; Mismatches 36; Indels 86; Gaps 12;
QY 29 PCHGDSSECKS---SPRCKRTVLDGCG-----GGLRCQPSN-GEDPFG-EPGI-- 99
DB 820 PRCDPCQCSGEGSLAVCD-TVTGQPCROGAHGRCDRCQCPGHWFPTCRQCQNGHA 878
QY 63 E-----TCYRTVSGMDGKMC-----GGLRCQPSN-GEDPFG-EPGI-- 99
DB 879 EECDDPQSGCLRCRDHTDGERCQRCAGHFGNPAISGQHCPCPCPDGPGGRHFAASC 938
QY 99 -----CKDCPYGTG-----GMDCRETCNCSGI-----CDR 124
DB 939 YDGRSRQVVCSPGYGTGPRCDECAPGYDPLQPGHGR-PCQCHNNIDTTDPEACDR 997
QY 125 GTCKCLK 131
DB 998 RTGQCLR 1004
PRT; 1645 AA.
PRELIMINARY;
ID O15230
AC O15230;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE KIAA0533 PROTEIN (LAMININ ALPHA 5 CHAIN) (FRAGMENT).
GN KIAA0533 OR LAMA5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BRAIN;
RX MEDLINE: 98290545.
RA NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N.,
RA OHARA O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RL code for large proteins in vitro.";
RN DNA RES. 5:31-39(1998).
RP SEQUENCE OF 693-1645 FROM N.A.

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RC TISSUE=PLACENTA;
RX MEDLINE: 97415425.
RA DURKIN M.E., LOECHEL F., MATTEI M., GILPIN B.J., ALBRECHTSEN R.,
RA NEWER U.M.;
RT "Tissue-specific expression of the human laminin alpha5-chain, and
RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
RL FEBS LETT. 411:296-300(1997).
DR EMBL: AB011105; D1026389; -.
DR EMBL: Z95636; E317479; -.
DR PFAM: PF00054; laminin_G; 2.
FT NON_TER 1
SQ SEQUENCE 1645 AA; 178215 MW; A44DE58F CRC32;

Query Match 10.5%; Score 96.5; DB 2; Length 1645;
Best Local Similarity 30.1%; Pred. No. 0.015;
Matches 28; Conservative 12; Mismatches 20; Indels 33; Gaps 6;

QY 48 LDGCGGCRVCAAGRGTCYRTVSGMDGMKGP---GLRCOPSNGE-----DPFGEEFGIC 99
Db 11 FNGCGGCRPCA-----CGPAEGSECHPQSGQCHCRPGTGMGPQ---C 49

QY 100 KCPYGTFGM---DCRETCNCQSGICDRGTGK 129
Db 50 RECAPGYWGLPEQGCR-RCQCPGGRCDPHTGRC 81

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Search completed: May 5, 1999, 08:18:42
Job time: 3115 sec